

**Supplementary Table 1:** Pairwise ILD P-values

Partition	Coding	pos1	pos2	pos3	pos1&2	Cons non-coding
<b>Coding</b>						<0.001
<b>Coding pos1</b>			0.323	<0.001		0.460
<b>Coding pos2</b>		0.648		0.983		0.324
<b>Coding pos3</b>		0.569	0.960			<0.001
<b>Coding pos1&amp;2</b>						0.432
<b>Cons non-coding</b>	0.328	0.361	0.696	0.951	0.163	

Supplementary Table 1: Pairwise incongruence length difference P-values between different data partitions. Values above the diagonal are for nucleotide-coded data, and below the diagonal are for RY-coded data. All ILD tests were performed using PAUP\* and 1000 replicates of 10 random addition TBR swapped maximum parsimony trees.

**Supplementary Table 2:** Gapped ILD-tests

Coding sequence, nucleotide-coded

<= 2 gaps, >2 gaps 0.591

<= 3 gaps, >3 gaps 0.273

Coding sequence, RY-coded

<= 2 gaps, >2 gaps 0.664

<= 3 gaps, >3 gaps 0.698

Conserved non-coding, nucleotide-coded

<= 3 gaps, >3 gaps 0.050

Conserved non-coding, RY-coded

<= 3 gaps, >3 gaps 0.627

Supplementary Table 2: ILD test results comparing positions with more gaps to those with few or no gaps. All ILD tests were performed using PAUP\* and 1000 replicates of 10 random addition TBR swapped maximum parsimony trees.